AMENDMENTS TO THE SPECIFICATION:

Please amend the specification as follows:

Please replace page 44, lines 36-37, with the following:

Figure 1: Synthesis of the linear ECDAB-OMe pentasaccharide **101** from the compounds **104**, **109**, **113** and **114** according to steps a) to j).

Figure 2: Retrosynthetic analysis of pentasaccharide **102** implying the synthons **118**, **119** and **113**.

Please replace page 45, line 3, with the following:

Figure 4: Synthesis of the AB(E)CD pentasaccharide **102** from compound **127**, via compounds **128**, **120**, **105**, **125**, **129**, **130**, **131**, **132**, **133**, and **134** according to steps a) to j).

Please replace page 45, lines 7-16, with the following:

Figure 8: Synthesis of compound **208** from compound **204** via compounds **205**, **206**, and **207** according to steps a) to d).

Figure 9: Synthesis of compound **212** from compound **209** via compounds **210** and **211** according to steps a) to c).

Figure 10: Synthesis of the pentasaccharide **203**, via compounds **214**, **212**, **215**, **216**, **217**, **218**, and **208** according to steps a) to f).

Figure 11: Retrosynthetic analysis of the target decasaccharide D'A'B'(E')C'DAB(E)C **301** according to various routes (a), (b) and (c). Route (a): involving synthons **306** to **310**; Route (b): involving synthons **311** to **313**.

Figure 12: Synthesis of the pentasaccharides **302, 303, 304** according to steps a) to e) or f) and involving notably a coupling with a trisaccharide **309** or **310** (see Figure 11).

Figure 13: Synthesis of the pentasaccharide **313** from monosaccharide **314** via compounds **321**, **322**, **323**, **316**, and **324-329** according to steps a) to h).

Figure 14: Synthesis of the tetrasaccharides **338, 339, 340, 341** according to steps a) to e) from compound **323** via compounds **311**, **332**, **333**, **334**, **335**, and **336** according to steps a) or b), c) to e).

Figure 15: Synthesis of the pentasaccharide **346** according to steps a) to f), from compound **311**, via compounds **321**, **342**, **310**, **343**, **344**, **340**, **304**, and **345** according to steps a) to f).

Figure 16: Synthesis of the decasaccharide D'A'B'(E')C'DAB(E)C **301** from compound **302** via compounds **347**, **348**, **346**, **349**, **350**, **351**, and **352** according to steps a) to g).

Please replace page 45, lines 18-23, with the following:

Figure 18: Synthesis of the hexasaccharide **402** according to steps e) to l) from compound **407** via compounds **408**, **406**, **405**, **409**, **410**, and **411**.

Figure 19: Retrosynthetic analysis of the target conjugates **501, 502, 503** involving the coupling of synthons **504**, **505**, or **506** with **507** and then with **508** via a reaction with SAMA-Pfp.

Figure 20: Synthesis of the aminoethyl ECD building block **518** from compounds **509** and **510**, via compounds **511**, **504**, **512**, **513**, **514**, **507**, **515**, **516**, and **517** according to steps a) to h).

Figure 21: Synthesis of the aminoethyl tetrasaccharide **525** from compound **511**, via compounds **519**, **520**, **521**, **522**, **505**, **507**, **523**, and **524** according to steps a) to g).

Figure 22: Synthesis of the aminoethyl pentasaccharide **537** from the compound **533**, via compounds **534**, **506**, **507**, **535**, and **536** according to steps f), c), g), h) and i), the compound **533** being obtained either from compound **526** via **527-530** according to steps a) to d) or from **519** via **532** and **527** according to steps e) and d).

Figure 23: Synthesis of the conjugates **501, 502, 503** from compounds **518**, **525**, or **537** via compounds **538**, **539**, **540** and **508** according to steps a) to c).

Please replace page 45, lines 25-29, with the following:

Figure 25: Synthesis of the pentasaccharides **606** from compound **609** according to step a) and synthesis of **607** from compound **609** via compounds **610-615** according to steps b) to h).

Figure 26: Synthesis of the decasaccharide **620** according to steps a) to f) from compounds **607** and **608**, and via compounds **616**, **617**, **606**, **618**, **619**, and **603**.

Figure 27: Synthesis of the pentadecasaccharide **625** according to steps a) to e) from compounds **617** and **607**, and via compounds **621**, **622**, and **606**.

Figure 28: Synthesis of the conjugates **701** to **713** from coupling of **701** to **706** with **707**, which is:

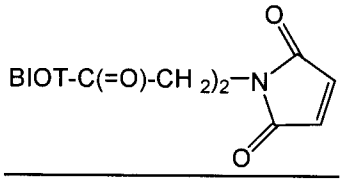

Figure 28bis: RetrosSynthesis of the conjugate **801**.

Please replace page 46, lines 30-33, with the following:

Figure 34 illustrates the protection conferred by oligosaccharides-tetanus toxoid conjugates in the mouse model of pulmonary infection. For each mice tested~~, the bacteria load 24 hours after the challenge is indicated as a function of~~ the antiLPS 2a antibody titer before the challenge (vertical axis) is indicated as a function of the bacteria load 24 hours after the challenge with tetra - (Fig 34 A), penta - (Fig 34 B), hexa - 35 (Fig 34 C), deca - (Fig 34 D), pentadecasaccharide (Fig 34 E) and LPS (Fig 34 F) conjugates (horizontal axis).

Please replace page 129, lines 1-21, with the following:

Total RNA was extracted from hybridoma cells by RNAxel kit (EUROBIO). mRNA was converted into cDNA with a reverse transcriptase kit (INVITROGEN) and used as template for PCR amplification using Taq DNA polymerase (GIBCO, BRL) according the manufacturer's protocol. The amplification was performed with the primer of corresponding isotype (SEQ ID NO: 1 to 3; IgG1: 5' GCA AGG CTT ACT AGT TGA AGA TTT GGG CTC AAC TTT CTT GTC GAC 3'; IgG2a: 5' GTT CTG ACT AGT GGG CAC TCT GGG CTC 3'; IgG3: 5'GGG GGT ACT AGT CTT GGG TAT TCT AGG CTC 3'. The following eight heavy chain variable region (VH) primers were also used (SEQ ID NO: 4 to 11: 5' GAG GTG CAG CTC GAG GAG TCA GGA CC3' ; 5' GAG GTC CAG CTC GAG CAG TCT GGA CC 3' ; 5' CAG GTC CAA CTC GAG CAG CCT GGG GC 3' ; 5' GAG GTT CAG CTC GAG CAG TCT GGG GC 3' ; 5' GAG GTG AAG CTC GAG GAA TCT GGA GG 3' ; 5' GAG GTA AAG CTC GAG GAG TCT GGA GG 3' ; 5' GAA GTG CAG CTC GAG GAG TCT GGG GG 3' ; 5' GAG GTT CAG CTC GAG CAG TCT GGA GC 3 '). Nucleic acid sequences were carried out by GENOME EXPRESS S.A. using PCR products. Sequence analysis was performed with software package from the

Genetics Computer Group, Inc (Madison, WI), the Genebank (Los Alamos, NM) and EMBL (Heidelberg, Germany) databases. For the determination of the genes families, analysis of the nucleotide sequences was performed with the international ImMunoGeneTics database ~~(http://imgt.cines.fr)~~ (Lefranc, M.-P., 2003 *Nucleic Acids Res.*, 31,307-310).

Please replace page 134, lines 1-12, with the following:

Table G: Comparison of the sequences of SYA/J6 (SEQ ID NO: 12, 35 to 39) and F22-4 (SEQ ID NO: 12, 16, 20, 24, 28 and 32) CDRs*

VH	H1	H2	H3
	31 35	52abc	100a
SYA/J6	NYWMS	EIRLKSNNYATHYAESVKG	GGAVGAMDY
F22-4	NYWMS	EIRLKS**D**NYAT**Y**YAESVKG	PMDY~~DY~~

VH	L1	L2	L3
	27abcde 30	50 56	89 97
SYA/J6	RSSQSLLHSDGNTYLH	KVSNRFS	SQTTHVPT
F22-4	RSS**K**SLLHSDGITYL**Y**	**HL**SN**LA**S	AHNVELPRT

*Kabat numbering